

FIG. 1A

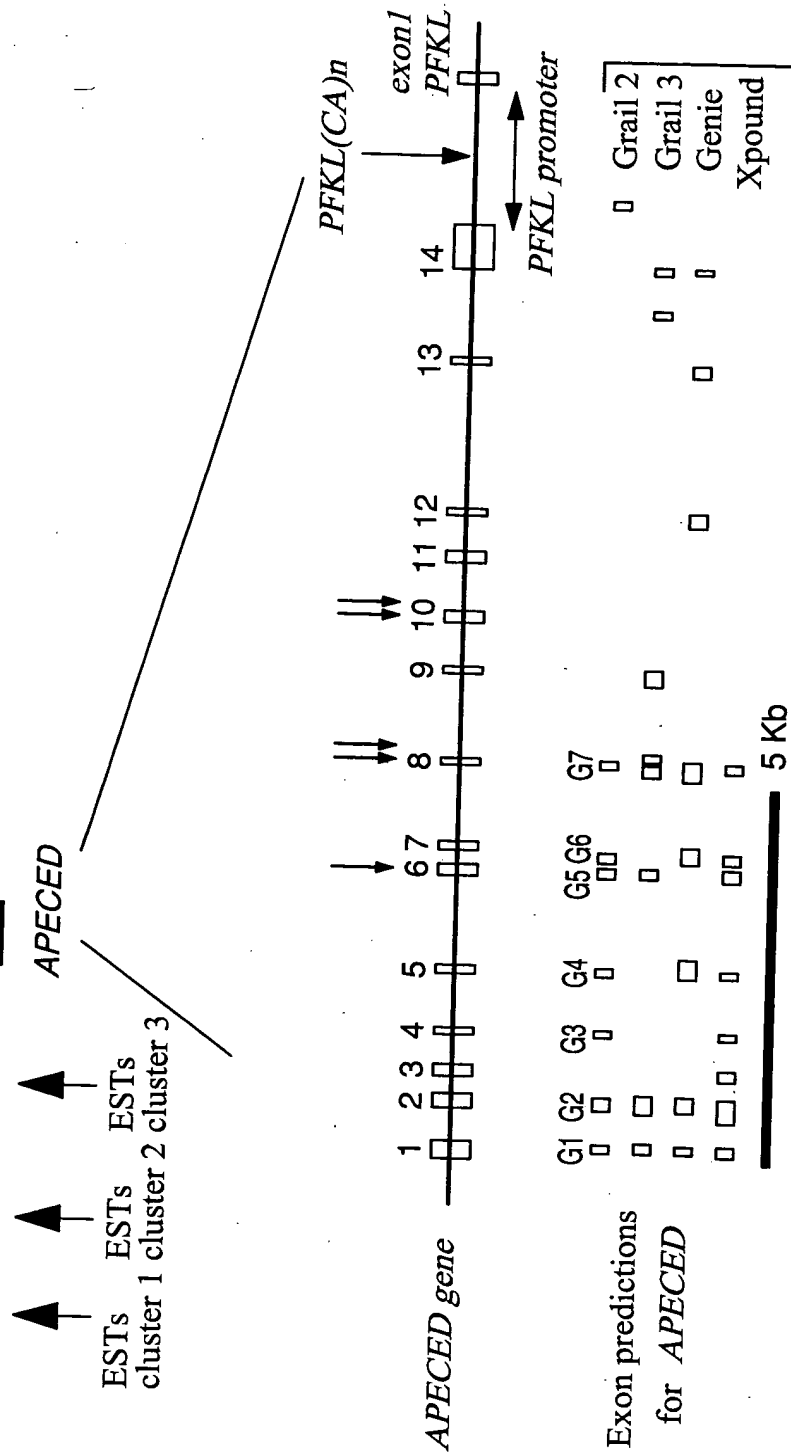


FIG. 1B

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Q11D11

Q21D1

cDNA B1-1

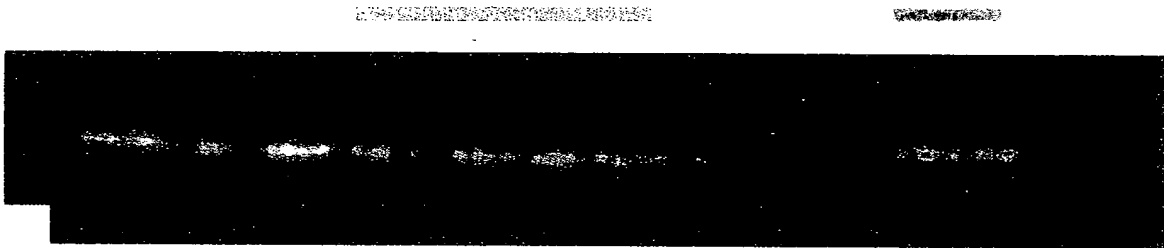


FIG. 1C

```

1  cgggcgcacagccggcgaggccccacagcccccgccgggaccccgaggccaagcgaggg 60
61  gctgccagtgctcccggaaccacccgctccgccccagccccgggtccccgcgccacccc 120
121 atggcgacggacgcgccgtacgcccgttctgaggctgcaccgcacggagatcgcggtg 180
1  M A T D A A L R R L L R L H R T E I A V 20
181 gccgtggacagcgccctccactgctgcacgcgctggctgaccacgacgtggtcccccgag 240
21  A V D S A F P L L H A L A D H D V V P E 40
241 gacaagtctcaggagacgcttcatctgaaggaaaaaggagggtgccccaggccttccac 300
41  D K F Q E T L H L K E K E G C P Q A F H 60
301 gccctcctgtcctggctgacctgacccaggactccacagccatcctggacttctggagggtg 360
61  A L L S W L L T Q D S T A I L D F W R V 80
361 ctgttcaaggactacaacctggagcgctatggccggctgcagccatcctggacagcttc 420
81  L F K D Y N L E R Y G R L Q P I L D S F 100
421 cccaaagatgtggacctcagccagccccgggaaggagggaagcccccgccgtccccaag 480
101 P K D V D L S Q P R K G R K P P A V P K 120
481 gctttgggtaccgcccaccagactccccaccaagagggaaggcctcagaagggtcgcagct 540
121 A L V P P P R L P T K R K A S E E A R A 140
541 gccgcgcagcagccctgactccaaggggcaccgccagccaggctctcaactgaaggcc 600
141 A A P A A L T P R G T A S P G S Q L K A 160
601 aagcccccaagaagcgggagagcagcgagcagcagcagcgcccttccactcgggaacggg 660
161 K P P K K P E S S A E Q Q R L P L G N G 180
661 attcagaccatgtcagcttcagttccagagagctgtggccatgtctcctccgggacgtcccg 720
181 I Q T M S A S V Q R A V A M S S G D V P 200

```

FIG. 2A-1

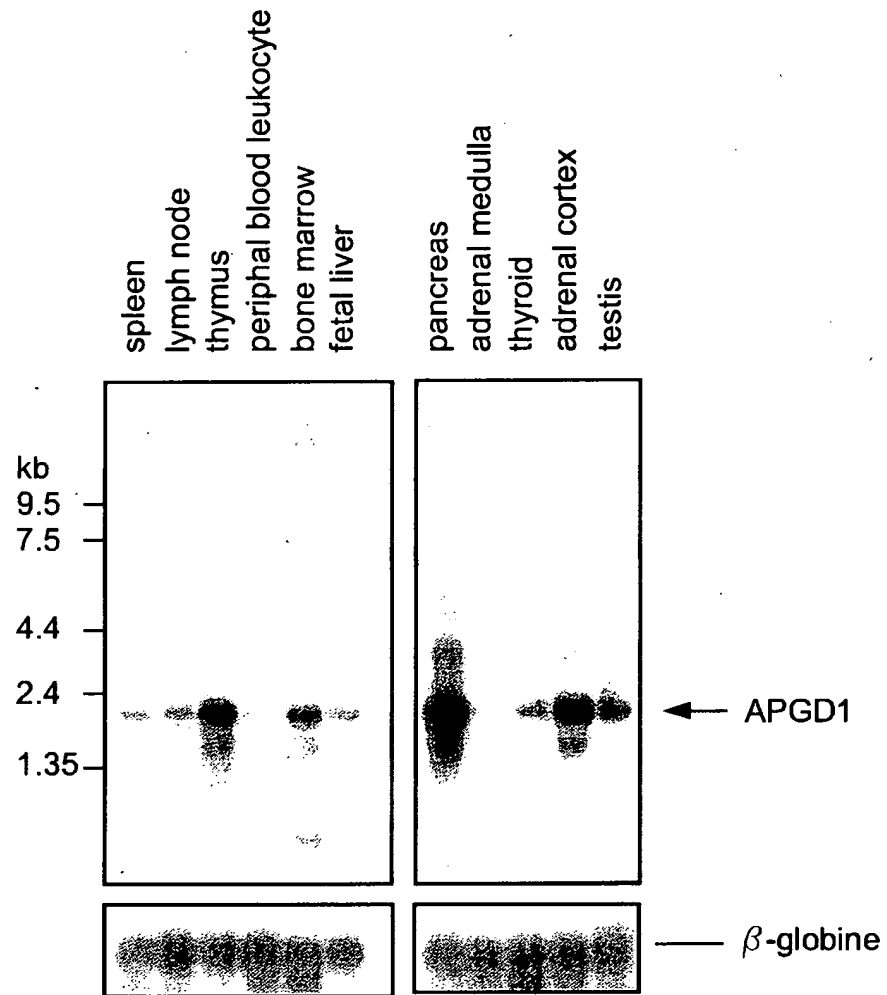
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721	ggagcccgagggccgtggaggggatcctcatccagcaggtgtttagtcaggcggctcc	780
201	G A R G A V E G I L I Q Q V F E S G G S	220
781	aagaagtgcattccaggttgggtgggagttctacactccagcaagtctcgaagactccggc	840
221	K K C I Q V G G E F Y T P S K F E D S G	240
841	agtgggaagaacaaggcccgagcagcagtgggccgaagcctctgtgttcgagccaagga	900
241	S G K N K A R S S S G P K P L V R A K G	260
901	gcccagggcgctgcccccggtggaggtaggtggccagcagggcagcggttccc	960
261	A Q G A A P G G G E A R L G Q Q G S V P	280
961	gcccccttggccctcccaagtgaacccagctccaccagaagaatgaggacgagtgtgcc	1020
281	A P L A L P S D P Q L H Q K N E D E C A	300
1021	gtgtgtcgggacggggagctcatctgtgtgacggctgccctcgggccttccacctg	1080
301	V C R D G G E L I C C D G C P R A F H L	320
1081	gcctgcctgtccccctcgctccgggagatccccagtgggacctggaggtgctccagctgc	1140
321	A C L P P L R E I P S G T W R C S S C	340
1141	ctgcaggcaacagtcaggaggtgcagccccgggcagaggagccccccagggagcca	1200
341	L Q A T V Q E V Q P R A E E P R P Q E P	360
1201	cccgtggagacccccgcctccccccgggcttaggtcggcgaggagaggttaagaggtcca	1260
361	P V E T P L P P G L R S A G E E V R G P	380
1261	cctggggaacccctagccggcatggacacgactcttgtctacaagcacctgcccgtccg	1320
381	P G E P L A G M D T T L V Y K H L P A P	400
1321	ccttctgcagccccgcgtgccagggtggactcctcgccctgcacccccctactgtgtg	1380
401	P S A A P L P G L D S S A L H P L L C V	420

FIG. 2A-2

FIG. 2A-3

2221 tcagtggcattcacatctcatgtaa 2245

**FIG. 2B**

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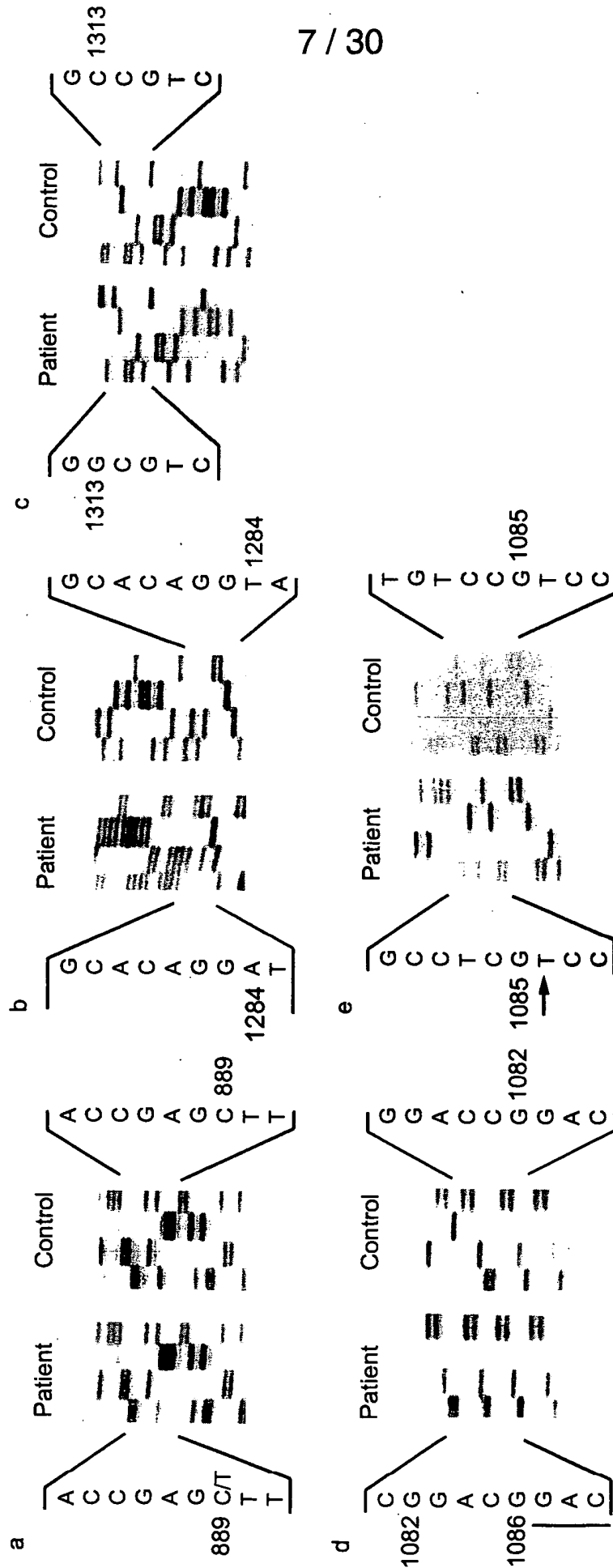


FIG. 3

The sequence lanes appear from left to right, as C, A, T, and G

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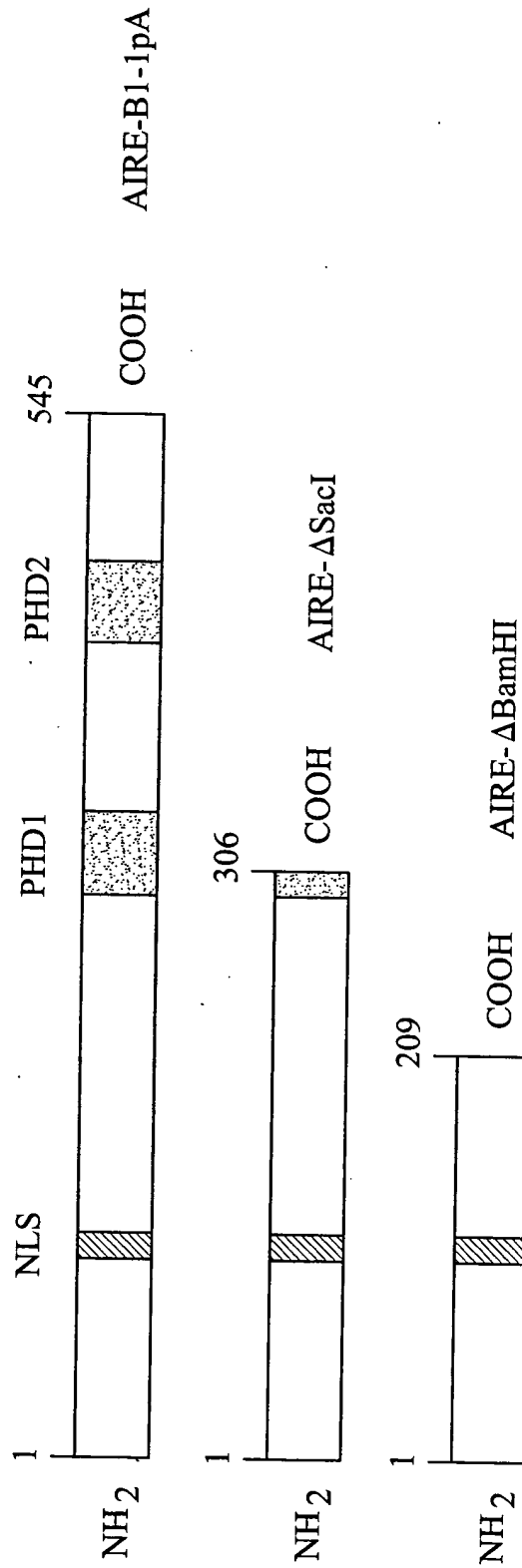


FIG. 4

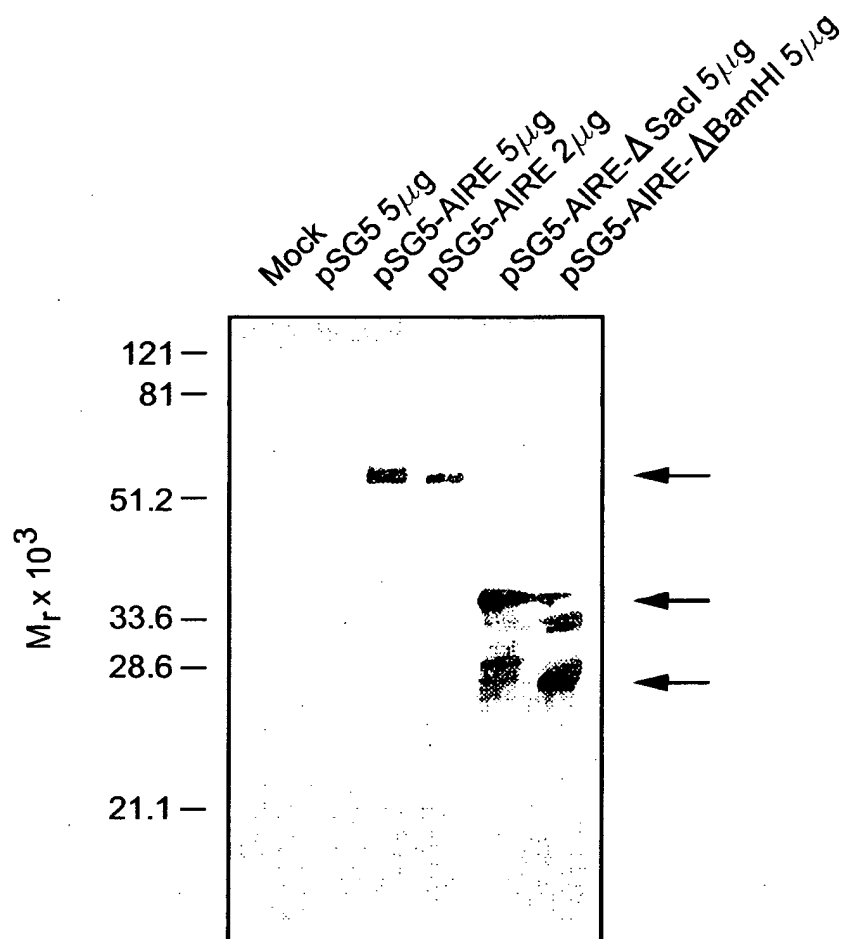


FIG. 5

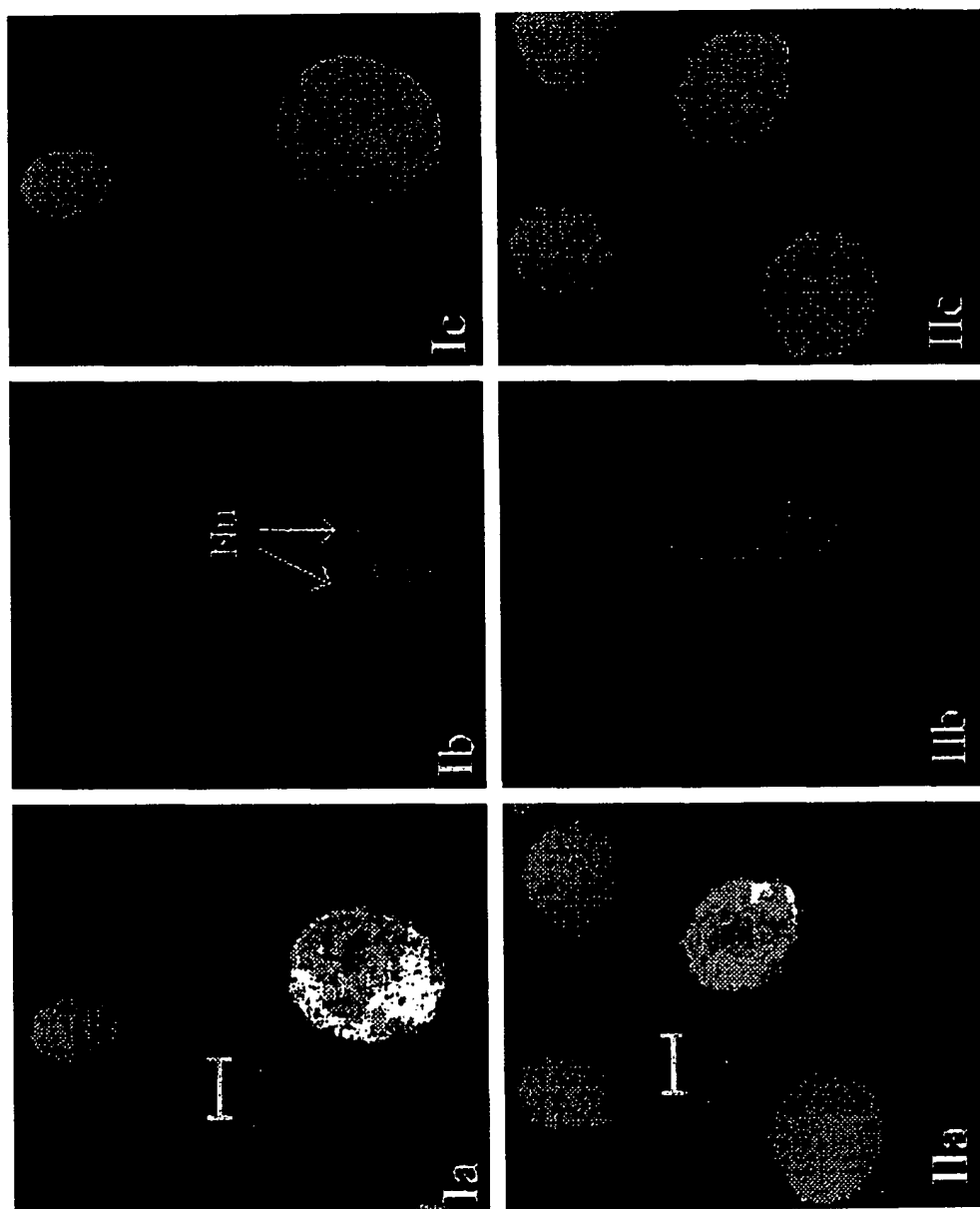


FIG. 6

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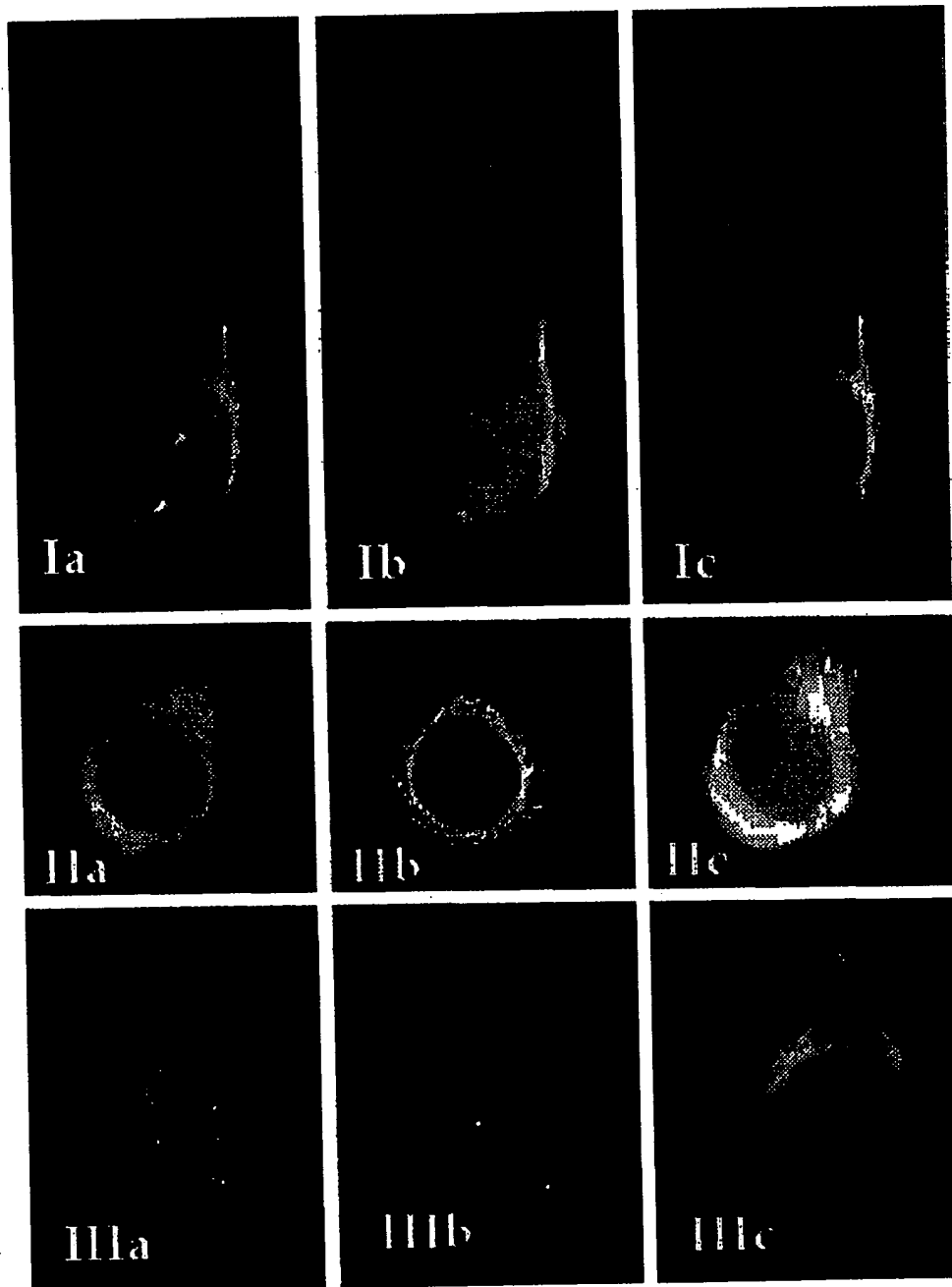


FIG. 7

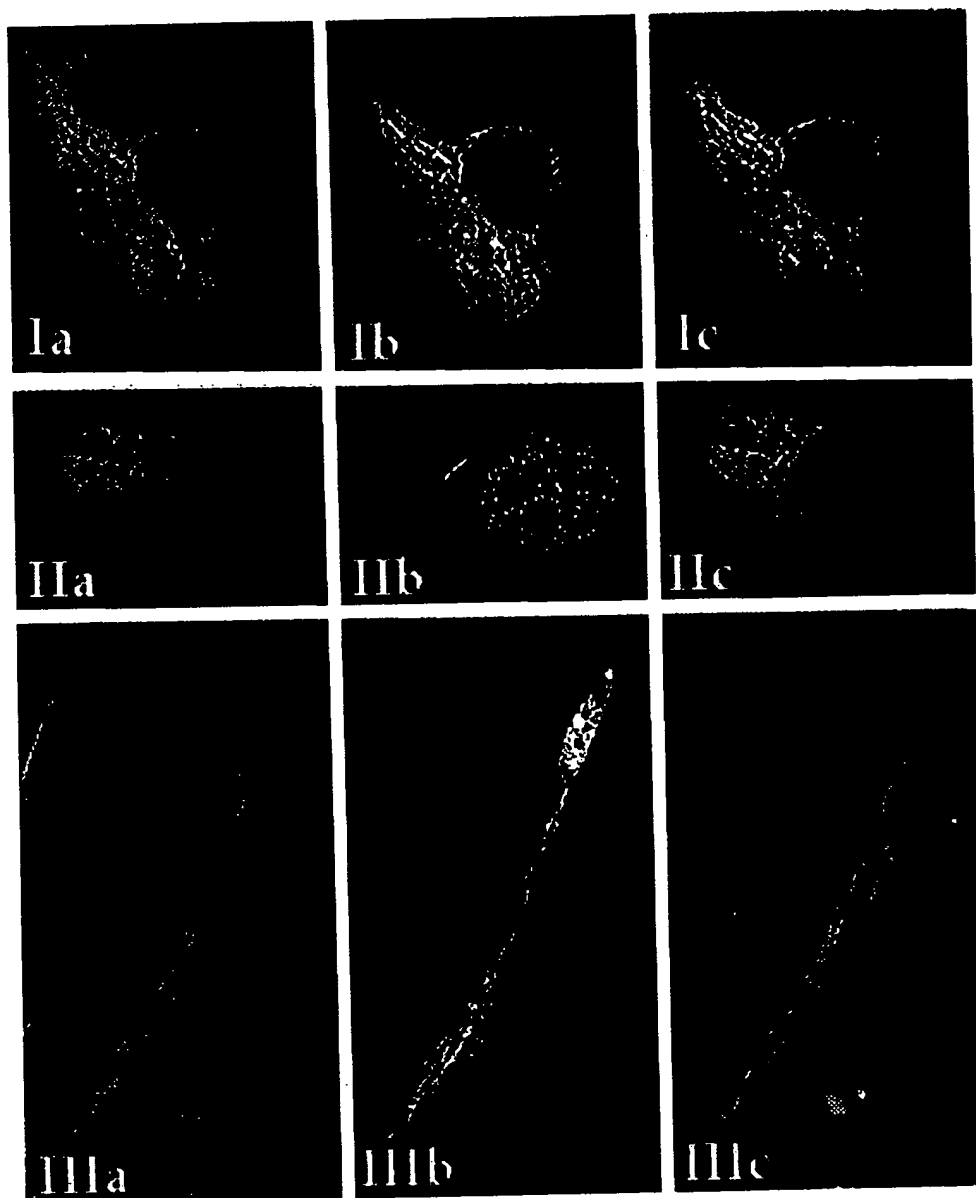


FIG. 8

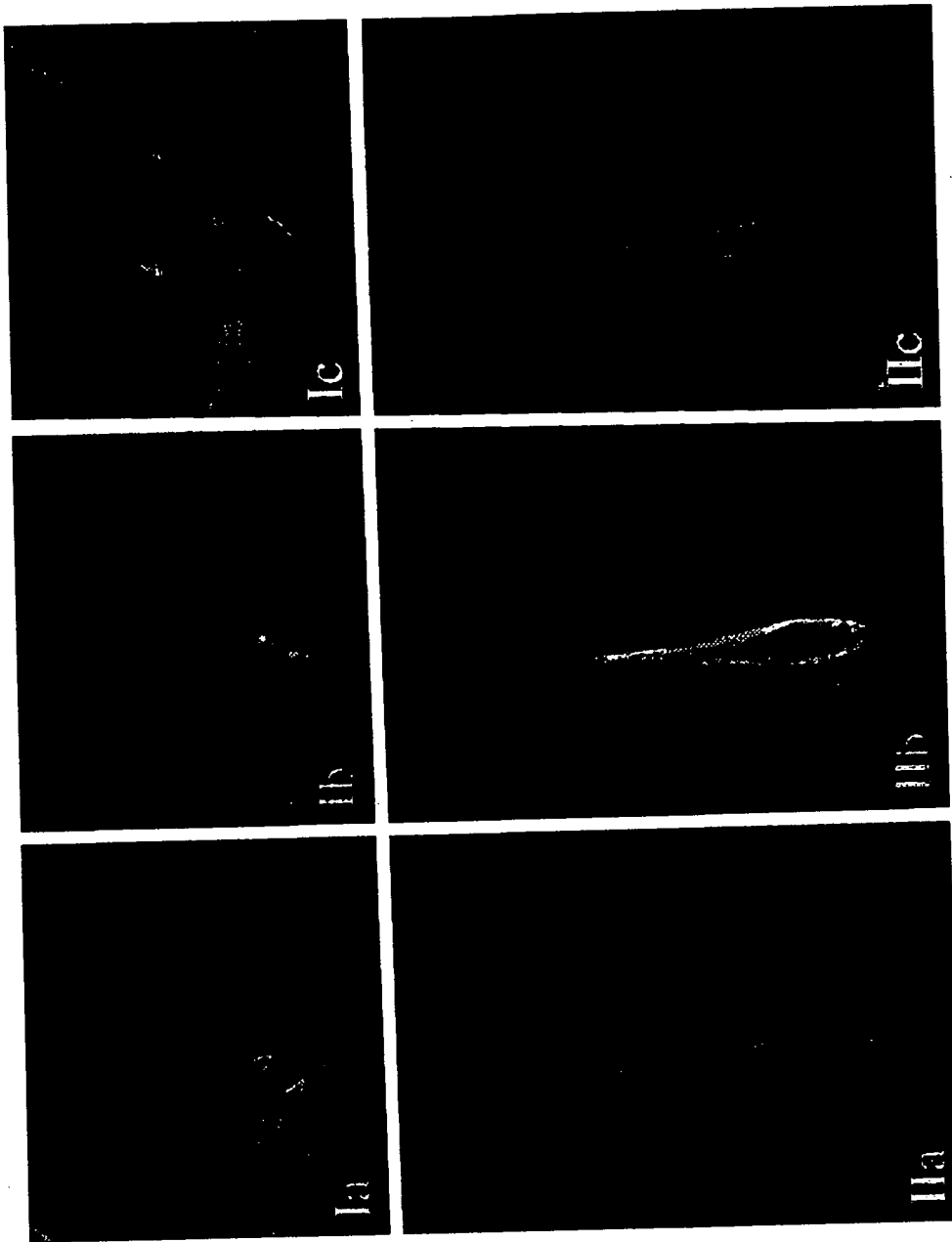


FIG. 9

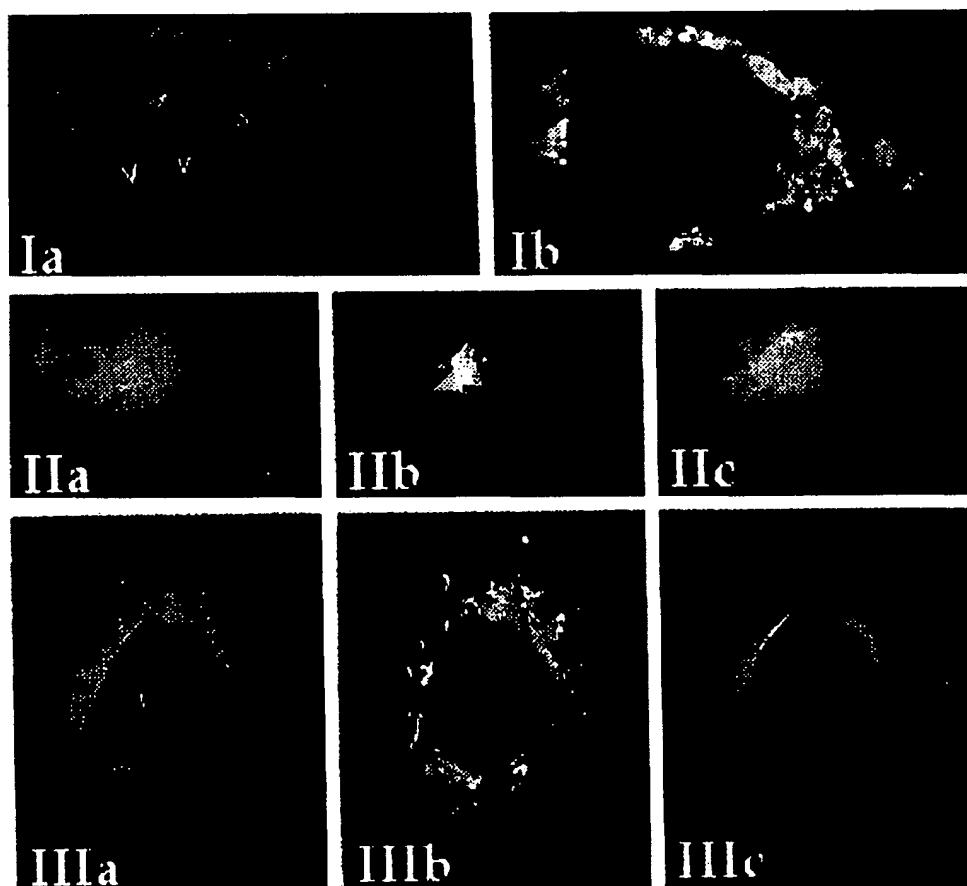


FIG. 10

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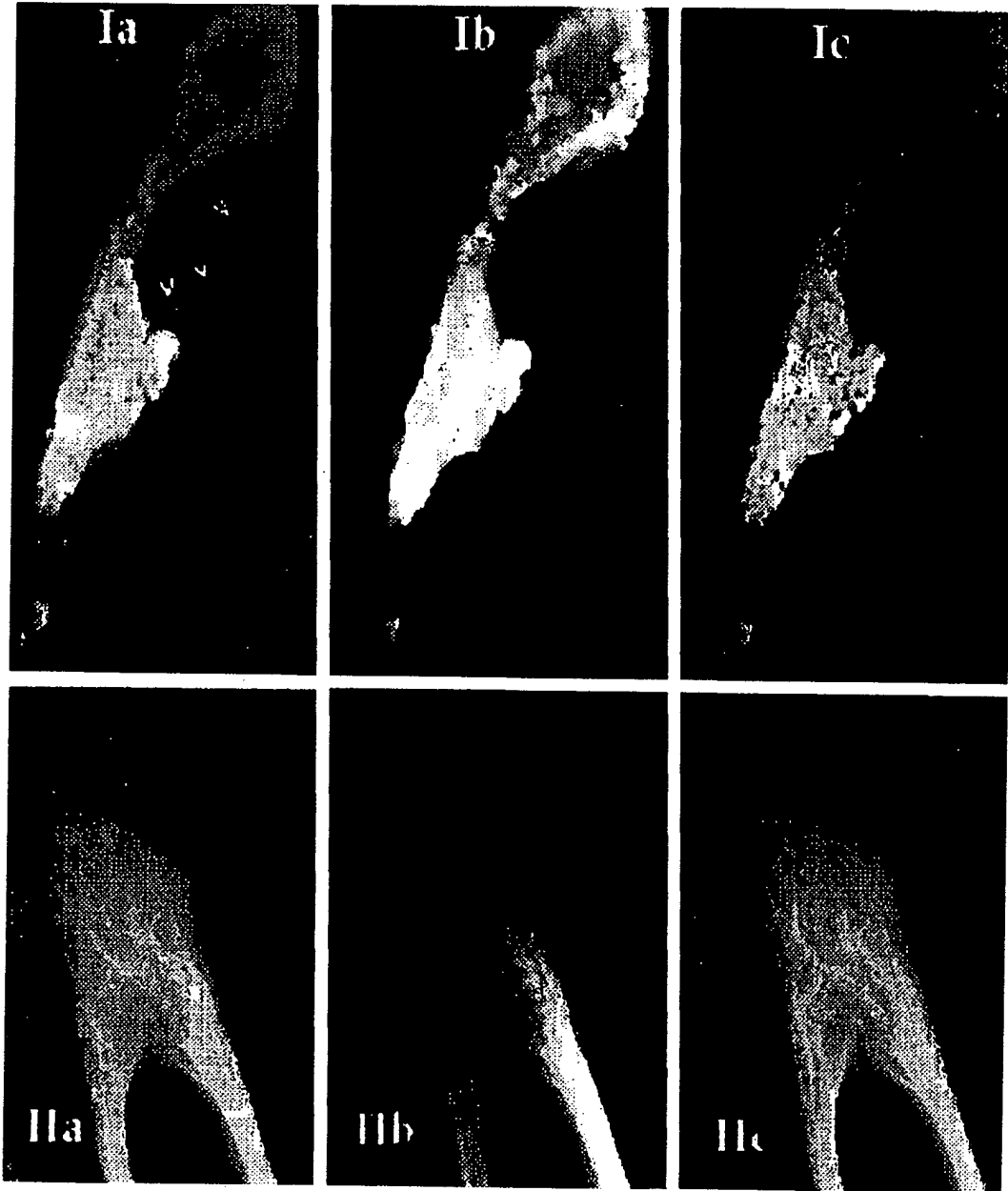


FIG. 11

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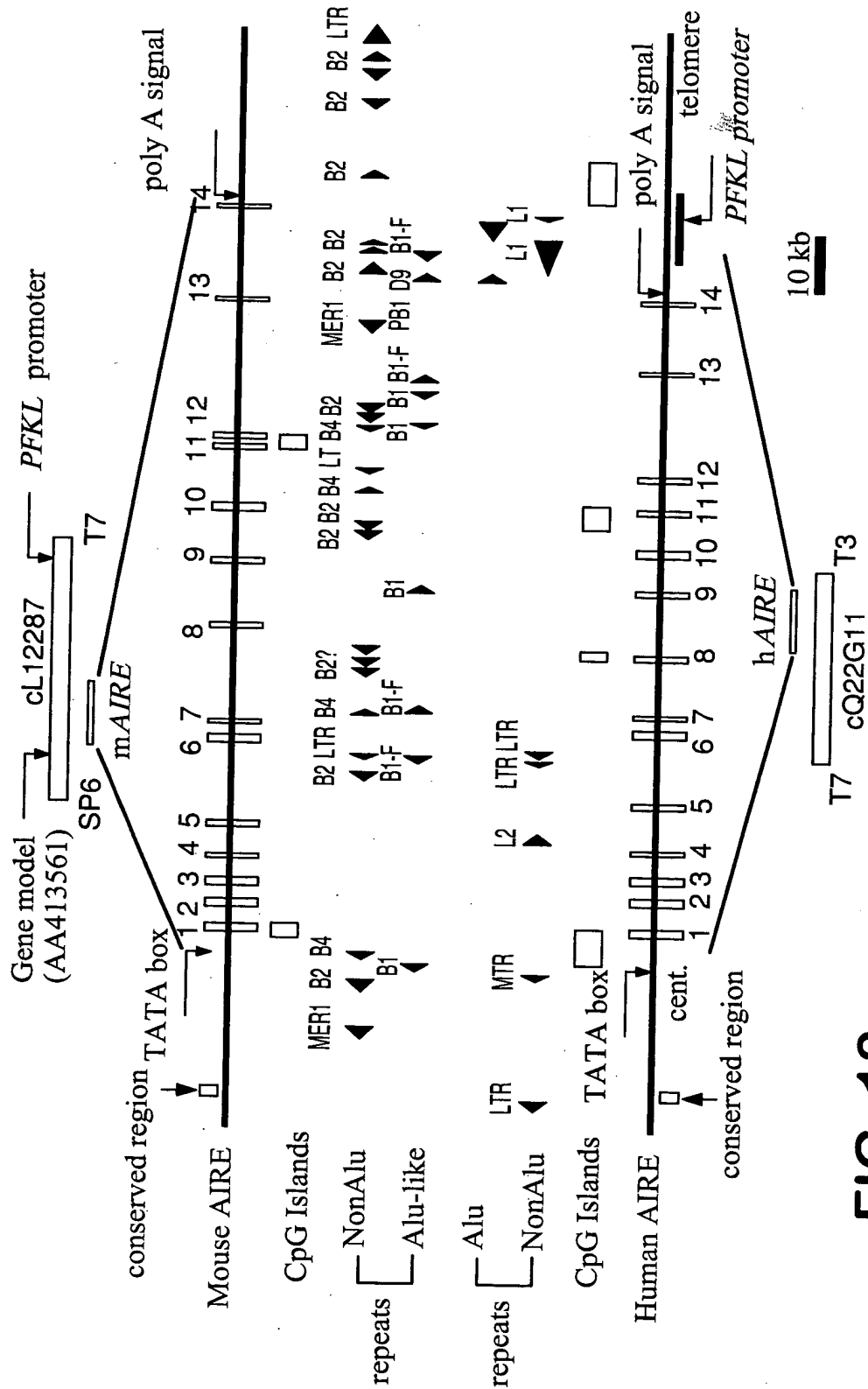


FIG. 12

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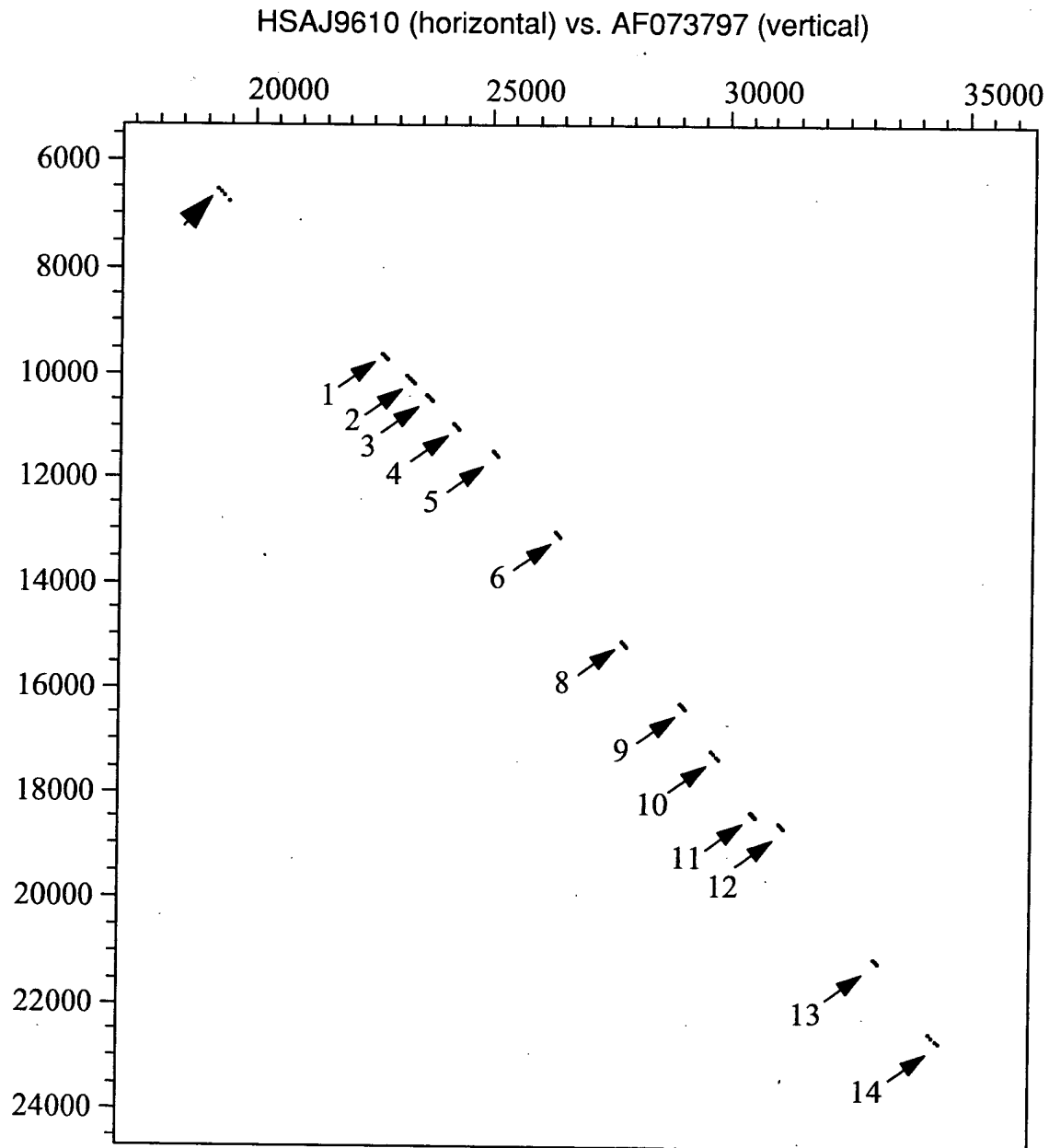


FIG. 13A

---G-GG---G T---G-AA-C CCC---G--T G-TGGAAGT

mAIRE	CCAAAAATTCT	ACAGGAGTCT	TTCTGTTGAT	CTCCAGTCAG	AGGCTGGGGG	6575
hAIRE	CCGAAATTCT	ACAGGGGCCT	CTTTGTTAAA	CCTCCATGCA	AGAGGCTGGG	19275
	CC-AAAATTCT	ACAGG-G-CT	-T-TGTT-A-	C--C--T---	AG-----GGG	

FIG. 13B

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```

10      30      50
1  ATGGCAGGTGGGATGGAATGCTACGCCGTCTGCTGAGGCTGCACCGCACCGAGATCGCG 60
-----+-----+-----+
1  M A G G D G M L R R L L R L H R T E I A 20
70      90      110
61 GTGGCCATAGACAGTGCCTTTCCGCTGCTGCATGCTCTAGCCGACCGACGTGGTCCCT 120
-----+-----+-----+
21 V A I D S A F P L L H A L A D H D V V P 40
130      150      170
121 GAGGACAAAGTTCCAGGAGACGCTCCGCTCTGAAGGAGAAGGAAGGCTGCCCCAGGCCTTC 180
-----+-----+-----+
41 E D K F Q E T L R L K E K E G C P Q A F 60
190      210      230
181 CACGCCCTGCTGCTCCTGCTCCTGACCCGGGACAGTGGGCCATCCTGGATTCTGGAGG 240
-----+-----+-----+
61 H A L L S W L L T R D S G A I L D F W R 80
250      270      290
241 ATTCTCTTTAAGGACTACAAATCTGGAGCGGTACAGCCGCCCTGCATAGCATCCTGGACGGC 300
-----+-----+-----+
81 I L F K D Y N L E R Y S R L H S I L D G 100
310      330      350
301 TTCCCAAAGATGTGGACCTAAACCAGTCCCGGAAAGGAGAAAGCCCTTGCTGGTCCC 360
-----+-----+-----+
101 F P K D V D L N Q S R K G R K P L A G P 120
```

FIG. 14-1

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```

370                               390                               410
361 AAGCGCGGTACTGCCACCCAGACCCCCACCAAGAGAAAGCACTGGAGAGCCTCGA 420
-----+-----+-----+-----+-----+-----+-----+-----+
121 K A A V L P P R P P T K R K A L E E P R 140
430                               450                               470
421 GCCACCCCAAGCAACTCTGGCCTCAAAGAGCGTCTCCAGCCCAGGCTCCCACCTGAAG 480
-----+-----+-----+-----+-----+-----+-----+
141 A T P P A T L A S K S V S S P G S H L K 160
490                               510                               530
481 ACTAAGCCCCCTAAGAAGCCAGATGGCAACTTGGAGTCACAGCACCTTCTTGGAAAC 540
-----+-----+-----+-----+-----+-----+-----+
161 T K P P K K P D G N L E S Q H L P L G N 180
550                               570                               590
541 GGAATTCAGACCATGGCAGCTTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGATGTT 600
-----+-----+-----+-----+-----+-----+-----+
181 G I Q T M A A S V Q R A V T V A S G D V 200
610                               630                               650
601 CCAGGAACCCGAGGGCCGTGGAAGGATCCTTATCCAGCAGGTGTTGAGTCAGGAAGA 660
-----+-----+-----+-----+-----+-----+-----+
201 P G T R G A V E G I L I Q Q V F E S G R 220
670                               690                               710
661 TCCAAGAAGTGCATTGAGTTGGGGAGAGTTTATACACCCCAAGTTCGAAGACCCC 720
-----+-----+-----+-----+-----+-----+-----+
221 S K K C I Q V G G E F Y T P N K F E D P 240

```

FIG. 14-2

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	730		750		770	
721	AGTGGCAATTGAGAACAAAGGCCCGAGTGGTAGCAGCCTAAAGCCAGTGGTCCGAGCC					780
241	S G N L K N K A R S G S S L K P V R A					260
	790		810		830	
781	AAGGGAGCCAGGTCACTATACCTGGTAGAGATGAGCAGAAAGTGGGCCAGCAGTGTGGG					840
261	K G A Q V T I P G R D E Q K V G Q Q C G					280
	850		870		890	
841	GTTCCCTCCCCTCCCATCCCTCCCCAGTGAGCCCCCAGGTTAACCCAGAAACGAGGATGAG					900
281	V P P L P S L P S E P Q V N Q K N E D E					300
	910		930		950	
901	TGTGCCGTGTGCCACGACGAGGTGAGCTCATCTGTTGTGACGGCTGTCCCGGCCCTTC					960
301	C A V C H D G G E L I C C D G C P R A F					320
	970		990		1010	
961	CACCTGGCTTGCCCTGTCCCCACCTCTGCAGGAGATCCCCAGTGGCCCTCTGGAGATGCTCC					1020
321	H L A C L S P P L Q E I P S G L W R C S					340
	1030		1050		1070	
1021	TGCTGCCCTCCAGGCAGAGTCCAAACAGAAACCTGTCCCAGCCTGAGGTGTCCAGGCCCCCG					1080
341	C C L Q G R V Q Q N L S Q P E V S R P P					360

FIG. 14-3

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1090	1110	1130	
1081	GAGCTACCTGCAGAGACCCCGATCCTCGTGGGACTGAGGTGAGTTCAGAGAAACCAGG		1140
361	E L P A E T P I L V G L R S A S E K T R		380
	1150	1170	1190
1141	GGCCCATCCAGGGAGCTCAAAGCCAGCTCTGATGCTGCTGCATATGTGAACCTGCTG		1200
381	G P S R E L K A S S D A A V T Y V N L L		400
	1210	1230	1250
1201	GCCCCGACCCCTGCAGCTCCTCTGCTGGAGCCTTCAGCACTGTGCCCTCTACTGAGTGCT		1260
401	A P H P A A P L L E P S A L C P L L S A		420
	1270	1290	1310
1261	GGGAATGAGGGGGCCAGGTCCAGCACCAAGCGCGGATGCAGTGTGTGGCGATGGC		1320
421	G N E G R P G P A P S A R C S V C G D G		440
	1330	1350	1370
1321	ACCGAGGTGTGCGGTGTCACACTGTGCGCGCTGCCTTCCACTGGCGCTGCCACTTCCCCG		1380
441	T E V L R C A H C A A A F H W R C H F P		460
	1390	1410	1430

FIG. 14-4

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```
1381 ACGGCCGCGCGCGCGGACCAATCTCGCTGCAATCCTGCTCTGCAGACTCGACT 1440
-----+-----+-----+-----+-----+-----+-----+
461 T A A A R P G T N L R C K S C S A D S T 480
1450 1470 1490

1441 CCCACGCCAGGCACACCGGGCGAAGCTGTACCCACCTCTGGGCCCCGTCACACCTGGG 1500
-----+-----+-----+-----+-----+-----+-----+
481 P T P G T P G E A V P T S G P R P A P G 500
1510 1530 1550

1501 CTTGCCAAGtagGGGACGACTCTGCTAGTCACGACCCCTGTTCTACATAGGGACGACCTG 1560
-----+-----+-----+-----+-----+-----+-----+
501 L A K V G D D S A S H D P V L H R D D L 520
1570 1590 1610

1561 GAGTCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCCATCCAGAGCATG 1620
-----+-----+-----+-----+-----+-----+-----+
521 E S L L N E H S F D G I L Q W A I Q S M 540
1630 1650

1621 TCACGCCCGCTGGCCGAGACACACCCCTTCTCTTCC 1656
-----+-----+-----+-----+-----+-----+-----+
541 S R P L A E T P P F S S 552
```

FIG. 14-5

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M 1 2 3 4 5 6

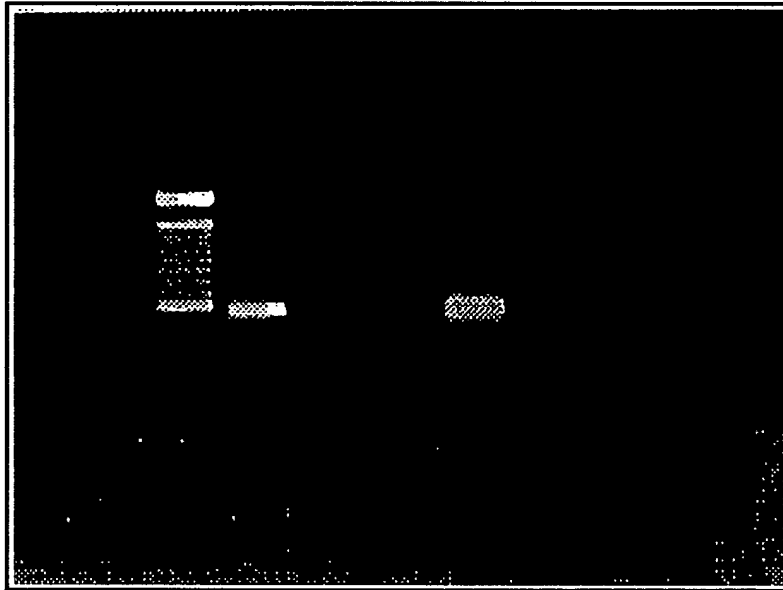


FIG. 15

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Human AIRE	-MATDAP	LRLRLRTEIA	VAVDSAFPLL	HALADHDVVP	EDKFQETLHL
Mouse AIRE	MAGGDGMLRR	LRLRLRTEIA	VAIDSAFPLL	HALADHDVVP	EDKFQETLRL
Consensus	----D--LRR	LRLRLRTEIA	VA-DSAFPLL	HALADHDVVP	EDKFQETL-L
Human AIRE	51	KEKEGCPQAF	HALLSWLLTQ	DSTAILDFWR	100
Mouse AIRE		KEKEGCPQAF	HALLSWLLTR	DSGAILDFWR	YGRLOPILDS
Consensus		KEKEGCPQAF	HALLSWLLT-	DS-AILDFWR	YRLHSILDG
Human AIRE	101	FPKDVDLSQP	RKGRKPPAVP	KALVPPPRLP	150
Mouse AIRE		FPKDVDLNQS	RKGRKPLAGP	KAAVLPPRPP	TKRKASEEAR
Consensus		FPKDVDL-Q-	RKGRKP-A-P	KA-V-PPR-P	TKRKA-EE-R
Human AIRE	151	GTASPGSQLK	AKPPKKPESS	AEQRLPLGN	200
Mouse AIRE		SVSSPGSHLK	TKPPKKPDGN	LESQHLPLGN	GIOTMSASVQ
Consensus		---SPGS-LK	-KPPKKP---	-E-Q-LPLGN	RAVAMSSGDV
Human AIRE	201	PGARGAVEGI	LIQQVFESGG	SKKCIQVGGE	250
Mouse AIRE		PGTRGAVEGI	LIQQVFESGR	SKKCIQVGGE	FYTPSKFED.
Consensus		PG-RGAVEGI	LIQQVFESG-	SKKCIQVGGE	FYTP-KFED-
Human AIRE	251	SSGPKPLVRA	KGAQGAAPGG	GEARLQQQGS	300
Mouse AIRE		GSSLKPVVRA	KGAQVTIPGR	DEQKVGQCG	VPAPLALPSD
Consensus		-S--KP-VRA	KGAQ---PG-	-E---GQQ--	VP--LPS-
					PQ--QKNEDE

FIG. 16-1

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Human AIRE	301	CAVCRDGGEL	ICCDGCPRAF	HLACLSPPLR	EIPSGTWRC	SCLQATVQEV	350
Mouse AIRE		CAVCHDGGEL	ICCDGCPRAF	HLACLSPPLO	EIPSGLWRC	CCLQGRVQON	
Consensus		CAVC-DGGEL	ICCDGCPRAF	HLACLSPPL-	EIPSG-WRC	-CLQ--VQ--	
Human AIRE	351	QPRAEPRPQ	EPVETPLPP	GLRSAGEVR	GPPGEPLAGM	DTTLVYKHL	400
Mouse AIRE		LSQPEVSRPP	ELPAETPILV	GLRSASEKTR	GPSRELKASS	DAAVTYVNL	
Consensus		----E--RP-	E-P-ETP---	GLRSA-E--R	GP--E--A--	D-----Y--L-	
Human AIRE	401	APPSAAPLPG	LDSSALHPLL	CVGPEGQONL	APGARCGVCG	DGTDVLRCTH	450
Mouse AIRE		APHPAAPL..	LEPSALCPLL	SAGNEGRPGP	APSARCSVCG	DGTEVLRCAH	
Consensus		AP--AAPL--	L--SAL-PLL	--G-EG----	AP-ARC-VCG	DGT-VLRC-H	
Human AIRE	451	CAAAFHWRCH	FPAGTSRPGT	GLRCRSCSGD	VTPAP.VEGV	LAP.SPARLA	500
Mouse AIRE		CAAAFHWRCH	FPTAAARPPT	NLRCKSCSAD	STPTPGTPE	AVPTSGPRPA	
Consensus		CAAAFHWRCH	FP----RPPT	-LRC-SCS-D	-TP-P---G-	--P-S--R-A	
Human AIRE	501	PGPAK...DDT	ASHEPALHRD	DLESLLSEHT	FDGILQWAIQ	SMARPAAPFP	550
Mouse AIRE		PGLAKVGDD	ASHDFVLHRD	DLESLLNEHS	FDGILQWAIQ	SMSRPLAETP	
Consensus		PG-AK--DD-	ASH-P-LHRD	DLESLL-EH-	FDGILQWAIQ	SM-RP-A--P	
Human AIRE	551	S---					
Mouse AIRE		PFSS					
Consensus		----					

FIG. 16-2

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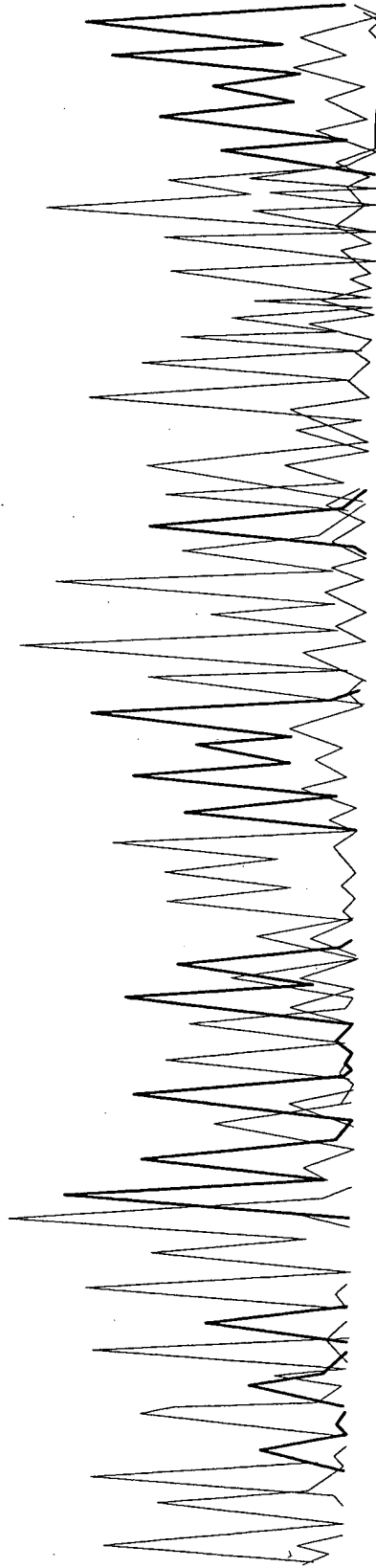
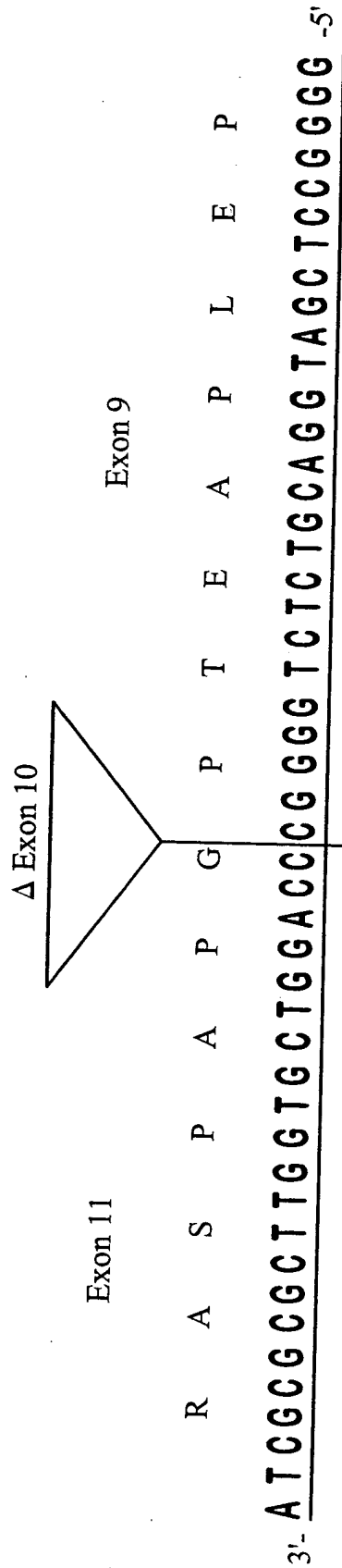


FIG. 17A

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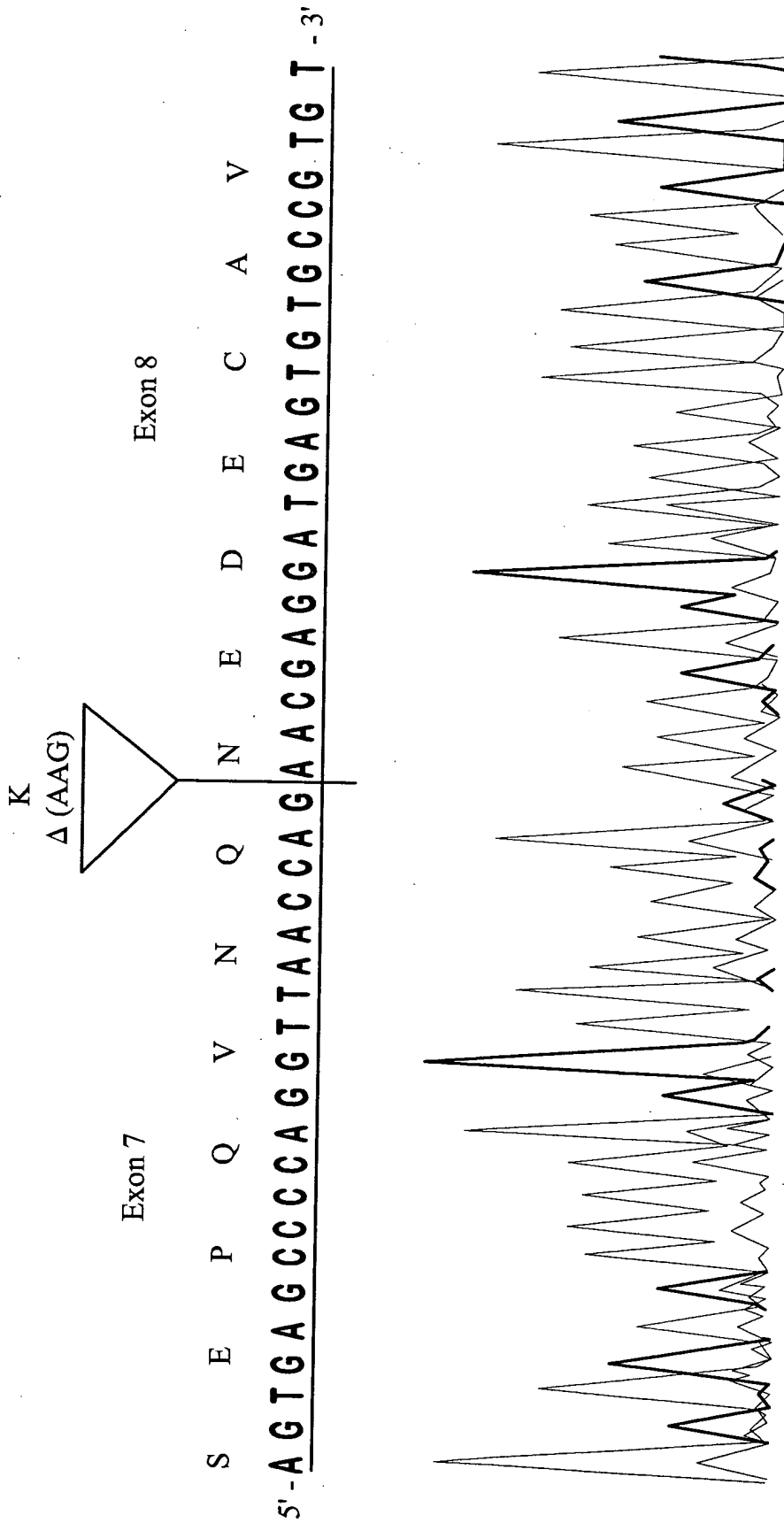


FIG. 17B

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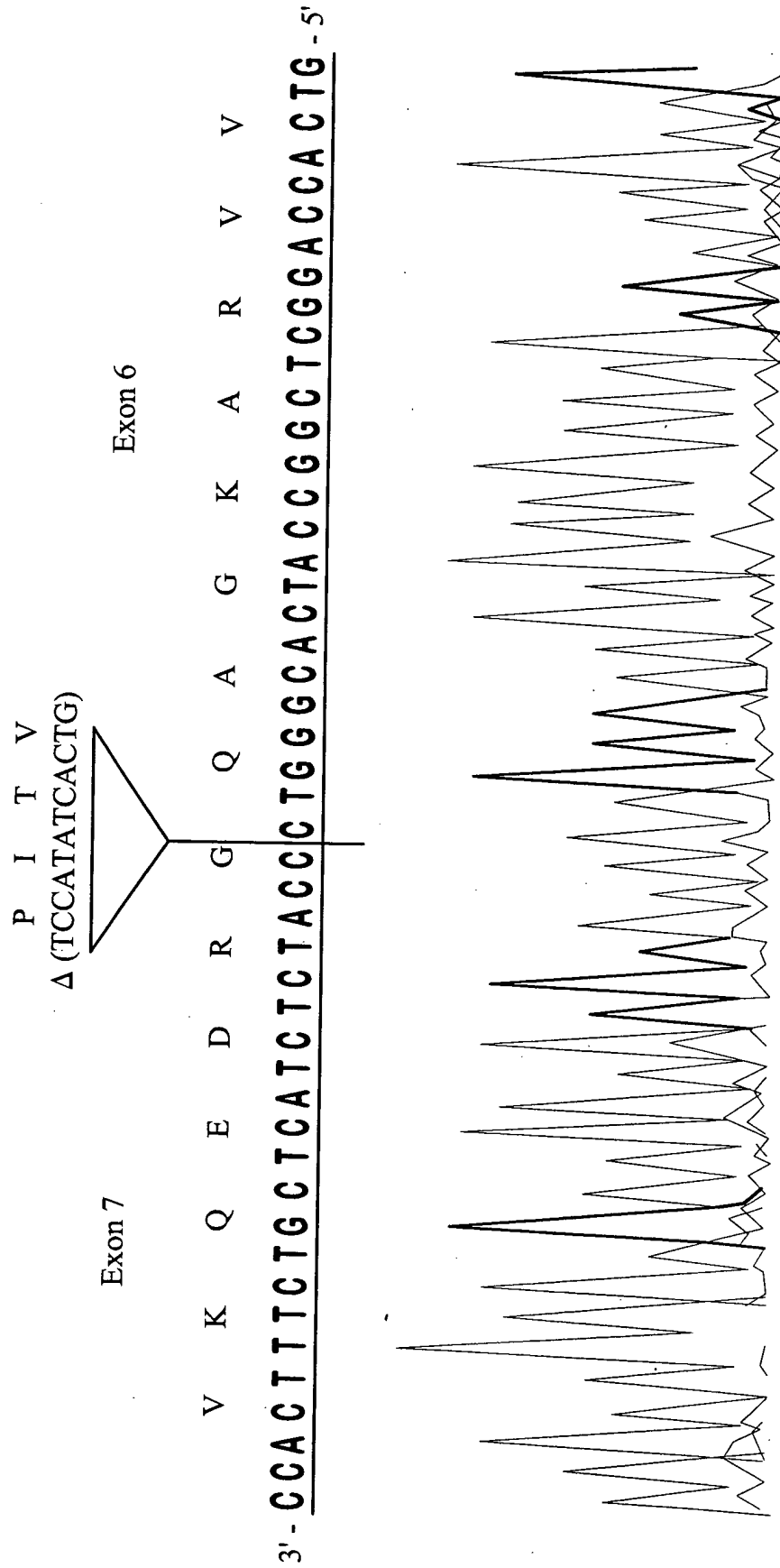


FIG. 17C

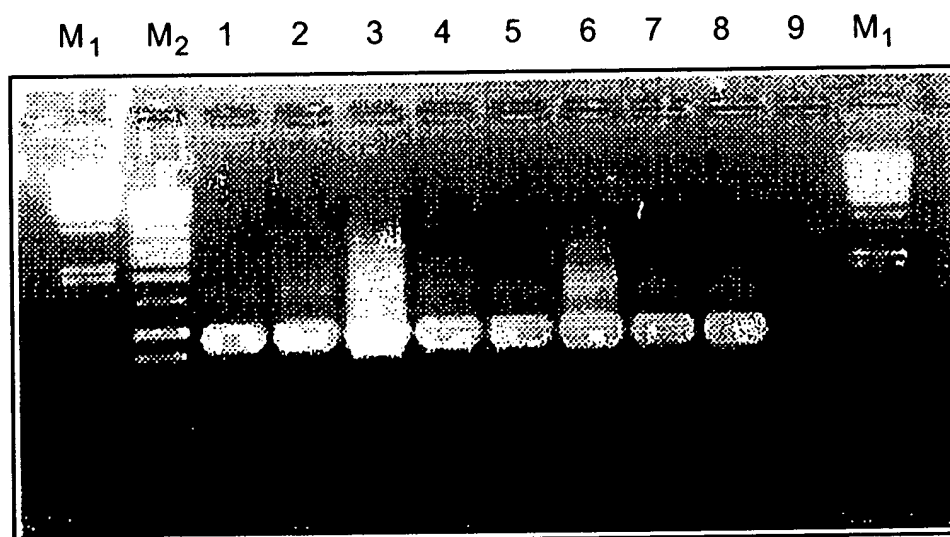


FIG. 18

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